

SEQUENCE LISTING

<110> MIYATA, Toshio

<120> A Method for Detecting Megsin Protein and Use
Thereof

<130> F2-101DP1PCT

<140>

<141>

<150> JP 1999-75305

<151> 1999-03-19

<150> JP 1999-306623

<151> 1999-10-28

<160> 21

<170> PatentIn Ver. 2.0

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (1140)

<300>

<302> A mesangium-predominant gene, megsin, is a new serpin
upregulated in IgA nephropathy.

<303> J. Clin. Invest.

<304> 120

<305> 4

<306> 828-836

<307> 1998-08-15

<400> 1

atg gcc tcc ctt gct gca gca aat gca gag ttt tgc ttc aac ctg ttc 48

Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe

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15

aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct 96

Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser

20

25

30

ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat 144

Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp

35

40

45

gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca 192

Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser

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gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg 240

Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu

65

70

75

80

aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc 288

Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu

85

90

95

agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag 336

Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys

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105

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gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga 384

Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg

115

120

125

gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag 432

Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys

130

135

140

tgg gtt gaa aat gaa aca cat ggc aaa atc aag aac gtg att ggt gaa 480

Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
 145 150 155 160

ggt ggc ata agc tca tct gct gta atg gtg ctg gtg aat gct gtg tac 528
 Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
 165 170 175

ttc aaa ggc aag tgg caa tca gcc ttc acc aag agc gaa acc ata aat 576
 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
 180 185 190

tgc cat ttc aaa tct ccc aag tgc tct ggg aag gca gtc gcc atg atg 624
 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
 195 200 205

cat cag gaa cgg aag ttc aat ttg tct gtt att gag gac cca tca atg 672
 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
 210 215 220

aag att ctt gag ctc aga tac aat ggt ggc ata aac atg tac gtt ctg 720
 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
 225 230 235 240

ctg cct gag aat gac ctc tct gaa att gaa aac aaa ctg acc ttt cag 768
 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
 245 250 255

aat cta atg gaa tgg acc aat cca agg cga atg acc tct aag tat gtt 816

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val

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gag gta ttt ttt cct cag ttc aag ata gag aag aat tat gaa atg aaa 864

Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys

275

280

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caa tat ttg aga gcc cta ggg ctg aaa gat atc ttt gat gaa tcc aaa 912

Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys

290

295

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gca gat ctc tct ggg att gct tcg ggg ggt cgt ctg tat ata tca agg 960

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg

305

310

315

320

atg atg cac aaa tct tac ata gag gtc act gag gag ggc acc gag gct 1008

Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala

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330

335

act gct gcc aca gga agt aat att gta gaa aag caa ctc cct cag tcc 1056

Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser

340

345

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acg ctg ttt aga gct gac cac cca ttc cta ttt gtt atc agg aag gat 1104

Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp

355

360

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gac atc atc tta ttc agt ggc aaa gtt tct tgc cct tga

1143

Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro

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<210> 2

<211> 380

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe

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Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser

20

25

30

Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp

35

40

45

Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser

50

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60

Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
65 70 75 80

Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
85 90 95

Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
100 105 110

Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
115 120 125

Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys
130 135 140

Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
145 150 155 160

Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
165 170 175

Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
180 185 190

Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
195 200 205

His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met

210

215

220

Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu

225

230

235

240

Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln

245

250

255

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val

260

265

270

Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys

275

280

285

Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys

290

295

300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg

305

310

315

320

Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala

325

330

335

Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser

340

345

350

Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp

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Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro

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375

380

<210> 3

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
synthesized degenerative primer sequence

<220>

<221> misc_feature

<222> 26, 29

<223> n is a or g or c or t.

<400> 3

gtgaatgctg tgtacttaaa ggcaantgn

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized degenerative primer sequence

<220>

<221> misc_feature

<222> 3, 9, 15

<223> n is a or g or c or t.

<400> 4

aanagraang grtcngc

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<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially

synthesized degenerative primer sequence

<220>

<221> misc_feature

<222> 6, 9, 12, 15, 18, 21

<223> n is a or g or c or t.

<400> 5

atggcntcng cngcngcngc naaygc

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<210> 6

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially

synthesized degenerative primer sequence

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cgacctccag aggcaattcc agagagatca gccctgg

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<210> 7

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized degenerative primer sequence

<400> 7

gtcttccaag cctacagatt tcaagtggt cctc

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<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized antisense primer sequence

<400> 8

gctcagggca gtgaagatgc tcaggaaga

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<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized antisense primer sequence

<400> 9

ctgacgtgca cagtcacctc gagcacc

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<210> 10

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized sense primer sequence

<400> 10

gaggtctcag aagaaggcac tgaggcaact gctgcc

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<210> 11

<211> 15

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 11

Phe Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe

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<210> 12

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 12

Ser Gln Ser Gly Leu Gln Ser Gln Leu Lys Arg Val Phe Ser Asp

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<210> 13

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 13

Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu

1 5 10 15

<210> 14

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 14

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val

1 5 10 15

<210> 15

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 15

Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu Phe Arg

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<210> 16

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 16

Leu Gly Leu Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp

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<210> 17

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 17

Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser Thr Val

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<210> 18

<211> 1229

<212> DNA

<213> Rattus norvegicus

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<221> CDS

<222> (8)..(1147)

<220>

<221> misc_feature

<222> 158, 159, 160, 287, 288, 289

<223> n is a or g or c or t.

<300>

<310> PCT/JP98/04269

<311> 1998-09-22

<400> 18

tttcaaa atg gcc tcc ctt gct gca gca aat gca gaa ttt ggc ttc gac 49

Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp

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tta ttc aga gag atg gat agt agt caa gga aac gga aat gta ttc ttc 97

Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe

15

20

25

30

tct tcc ctg agc atc ttc act gcc ctg agc cta atc cgt ttg ggt gct 145

Ser Ser Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala

35

40

45

cga ggt gac tgt nnn cgt cag att gac aag gcc ctg cac ttt atc tcc 193

Arg Gly Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser

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55

60

cca tca aga caa ggg aat tca tcg aac agt cag cta gga ctg caa tat 241

Pro Ser Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr

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70

75

caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag gat nnn 289

Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa

80

85

90

aaa ctc agc att gcc aat gga gtt ttt gca gag aaa gta ttt gat ttt 337

Lys Leu Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe

95

100

105

110

cat aag agc tat atg gag tgt gct gaa aac tta tac aat gct aaa gtg 385

His Lys Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val

115

120

125

gaa aga gtt gat ttt aca aat gat ata caa gaa acc aga ttt aaa att 433

Glu Arg Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile

130

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140

aat aaa tgg att gaa aat gaa aca cat ggc aaa atc aag aag gtg ttg 481

Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu

145

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ggg gac agc agc ctc agc tca tca gct gtc atg gtg cta gtg aat gct 529

Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala

160

165

170

gtt tac ttc aaa ggc aag tgg aaa tcg gcc ttc acc aag agt gat acc 577
Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr
175 180 185 190

ctc agt tgc cat ttc agg tct ccc agc ggt cct gga aaa gca gtt aat 625
Leu Ser Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn
195 200 205

atg atg cat caa gaa cgg agg ttc aat ttg tct acc att cag gag cca 673
Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro
210 215 220

cca atg cag att ctt gag cta caa tat cat ggt ggc ata agc atg tac 721
Pro Met Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr
225 230 235

atc atg ttg ccc gag gat gac cta tcc gaa att gaa agc aag ctg agt 769
Ile Met Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser
240 245 250

ttc cag aat cta atg gac tgg aca aat agc agg aag atg aaa tct cag 817
Phe Gln Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln
255 260 265 270

tat gtg aat gtg ttt ctc ccc cag ttc aag ata gag aaa gat tat gaa 865

Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu

275

280

285

atg agg agc cac ttg aaa tct gta ggc ttg gaa gac atc ttt gtt gag 913

Met Arg Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu

290

295

300

tcc agg gct gat ctg tct gga att gcc tct gga ggt cgt ctc tat gta 961

Ser Arg Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val

305

310

315

tca aag cta atg cac aag tcc ctc ata gag gtc tca gaa gaa ggc acc 1009

Ser Lys Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr

320

325

330

gag gca act gct gcc aca gaa agt aac atc gtt gaa aag cta ctt cct 1057

Glu Ala Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro

335

340

345

350

gaa tcc acg gtg ttc aga gct gac cgc ccc ttt ctg ttt gtc att agg 1105

Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg

355

360

365

aag aat ggc atc atc tta ttt act ggc aaa gtc tcg tgt cct 1147

Lys Asn Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

370

375

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tgaaattcta ttggttttc catacactaa caggcatgaa gaaacatcat aagtgaatag 1207

aattgtaatt ggaagtacat gg

1229

<210> 19

<211> 380

<212> PRT

<213> Rattus norvegicus

<220>

<221> misc_feature

<222> 51, 94

<223> Xaa is unknown.

<400> 19

Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp Leu Phe

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Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe Ser Ser

20

25

30

Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly

35

40

45

Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser

50

55

60

Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu

65

70

75

80

Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu

85

90

95

Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys

100

105

110

Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg

115

120

125

Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys

130

135

140

Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp

145

150

155

160

Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr

165

170

175

Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser

180

185

190

Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met

195

200

205

His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met

210

215

220

Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met

225

230

235

240

Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln

245

250

255

Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val

260

265

270

Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg

275

280

285

Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg

290

295

300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys

305

310

315

320

Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala

325

330

335

Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser

340

345

350

Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn

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365

Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

370

375

380

<210> 20

<211> 1147

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1104)

<300>

<310> PCT/JP98/04269

<311> 1998-09-22

<400> 20

ttc gac tta ttc aga gag atg gat agt agc caa gga aat gga aat gta 48

Phe Asp Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val

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15

ttc ttc tct tcc ctg agc atc ttc act gcc ctg acc cta atc cgt ctg 96

Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu

20

25

30

ggt gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt 144

Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe

35

40

45

aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt 192

Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu

50

55

60

cag tat caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag 240

Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys

65

70

75

80

gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat 288

Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr

85

90

95

gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct 336

Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala

100	105	110	
aaa gtg gaa aga gtt gac ttc aca aat gat gta caa gat acc aga ttt			384
Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe			
115	120	125	
aaa att aat aaa tgg att gaa aat gag aca cat gga aag atc aag aag			432
Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys			
130	135	140	
gtg ttg ggc gac agc agc ctc agc tcg tcg gct gtc atg gtg ctg gtg			480
Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val			
145	150	155	160
aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act			528
Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr			
165	170	175	
gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta			576
Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val			
180	185	190	
gtt aat atg atg cat caa gaa cgg cgg ttc aat ttg tct acc att cag			624
Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln			
195	200	205	

cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc 672

Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser

210

215

220

atg tac att atg ctg cct gag gat ggc cta tgt gaa att gaa agc aag 720

Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys

225

230

235

240

ctg agt ttc cag aat ctg atg gac tgg acc aat agg agg aaa atg aaa 768

Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys

245

250

255

tct cag tat gtg aac gtg ttt ctc ccc cag ttc aag ata gag aag aat 816

Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn

260

265

270

tat gaa atg acg cac cac ttg aaa tcc tta ggc ttg aaa gat atc ttt 864

Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe

275

280

285

gat gag tcc agt gca gat ctc tct gga att gcc tct gga ggt cgt ctc 912

Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu

290

295

300

tac gta tca aag cta atg cac aag tca ttc ata gag gtc tca gag gag 960

Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu

305

310

315

320

ggc act gaa gcc act gct gcc aca gaa aat aac att gtt gaa aag cag 1008

Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln

325

330

335

ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc 1056

Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val

340

345

350

atc aag aag aat gac atc atc tta ttt act ggc aaa gtc tct tgt cct 1104

Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

355

360

365

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20

25

30

Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe

35

40

45

Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu

50

55

60

Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys

65

70

75

80

Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr

85

90

95

Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala

100

105

110

Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe

115

120

125

Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys

130

135

140

Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val

145

150

155

160

Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr

165

170

175

Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val

180

185

190

Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln

195

200

205

Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser

210

215

220

Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys

225

230

235

240

Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys

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250

255

Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn

260

265

270

Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe

275

280

285

Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu

290

295

300

Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu

305

310

315

320

Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln

325

330

335

Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val

340

345

350

Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

355

360

365